

**results of BLAST****BLASTP 2.2.4 [Aug-26-2002]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1037910362-014405-16981

**Query=**

(150 letters)

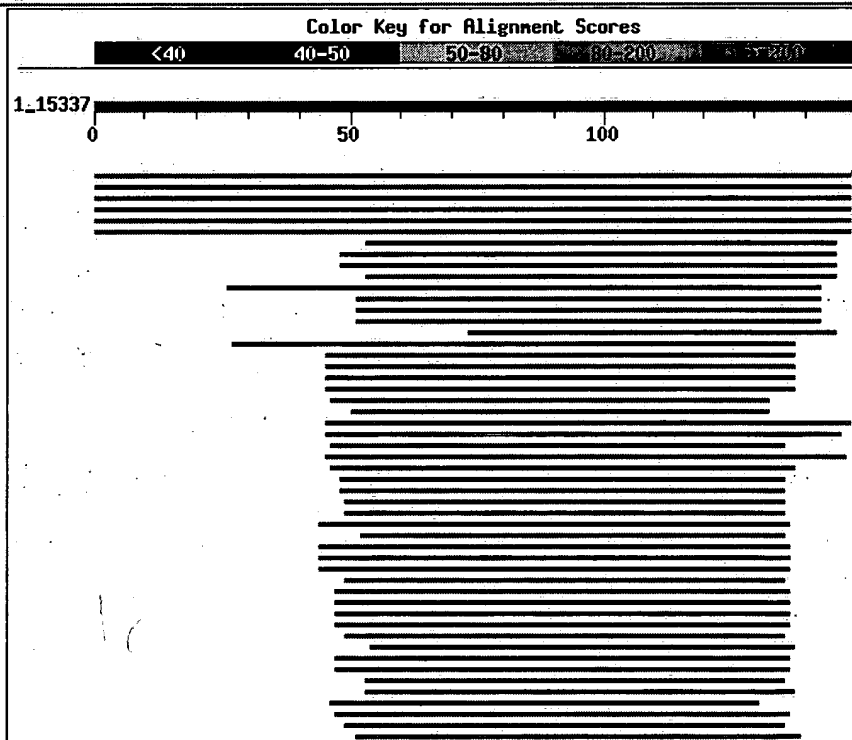
**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

1,242,147 sequences; 395,475,034 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 100 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments











Score E

## Sequences producing significant alignments:

(bits) Value

gi 20140248 sp Q9H2B4 S261 HUMAN	Sulfate anion transporter ...	234	4e-61	
gi 20336272 ref NP_071325.2	solute carrier family 26, memb...	233	4e-61	L
gi 20336274 ref NP_602297.1	solute carrier family 26, memb...	232	1e-60	L
gi 11560117 ref NP_071623.1	sulfate anion transporter [Rat...	197	4e-50	L
gi 19070535 gb AAL83908.1 AF349043.1	sulfate anion transpor...	196	6e-50	L
gi 20838541 ref XP_132232.1	similar to sulfate anion trans...	196	6e-50	L
gi 6746349 emb CAC69640.1	DTD sulfate transporter [Bos tau...	142	1e-33	
gi 627422 pir A54808	diastrophic dysplasia-associated sulf...	141	2e-33	
gi 4557539 ref NP_000103.1	sulfate anion transporter 1; Di...	141	2e-33	L
gi 12054717 emb CAC20729.1	sulfate transporter [Ovis aries]	140	5e-33	
gi 16923978 ref NP_476468.1	solute carrier family 26 (sulf...	136	7e-32	L
gi 12840625 dbj BAB24899.1	data source:MGD, source key:MGI...	136	7e-32	L
gi 6681233 ref NP_031911.1	solute carrier family 26 (sulfa...	135	1e-31	L
gi 20306204 gb AAH28345.1	solute carrier family 26 (sulfat...	135	1e-31	
gi 18560370 ref XP_087654.1	similar to Sulfate transporter...	119	1e-26	L
gi 23491578 dbj BAC16761.1	solute carrier family 26 member...	94	6e-19	
gi 20139418 sp P58743 PRES HUMAN	Prestin	93	8e-19	
gi 13540646 ref NP_110467.1	prestin [Rattus norvegicus] >g...	93	1e-18	L
gi 15011891 ref NP_109652.2	prestin (motor protein) [Mus m...	92	2e-18	L
gi 20139749 sp Q9JKQ2 PRES MERUN	Prestin >gi 8050590 gb AAF...	92	2e-18	
gi 17566848 ref NP_505493.1	sulphate permease [Caenorhabdi...	92	2e-18	L
gi 17570247 ref NP_509855.1	dra like protein [Caenorhabdit...	91	3e-18	L
gi 17551690 ref NP_508944.1	sulfate transporter [Caenorhab...	90	9e-18	L
gi 4557535 ref NP_000102.1	down-regulated in adenoma prote...	90	9e-18	L
gi 7499071 pir T16077	hypothetical protein F14D12.5 - Caen...	90	1e-17	
gi 17562578 ref NP_505989.1	sulphate transporter [Caenorha...	89	2e-17	L
gi 20137595 sp Q924C9 DRA RAT	Chloride anion exchanger (DRA...	88	3e-17	
gi 4505697 ref NP_000432.1	pendrin [Homo sapiens] >gi 6174...	87	8e-17	L
gi 6755022 ref NP_035997.1	pendrin; Pendred syndrome homol...	86	2e-16	L
gi 2626753 dbj BAA23424.1	sulfate transporter [Arabidopsis...	86	2e-16	
gi 15240652 ref NP_196859.1	sulfate transporter; protein i...	86	2e-16	
gi 9506965 ref NP_062087.1	pendrin; Pendred syndrome homol...	85	3e-16	L
gi 19705561 ref NP_599252.1	solute carrier family 26, memb...	85	3e-16	L
gi 22775307 gb AAL13129.1	anion exchanger SLC26A6a [Mus mu...	84	4e-16	L
gi 20810386 gb AAH28856.1	solute carrier family 26, member...	84	4e-16	L
gi 22773848 gb AAN07089.1 AF248494.1	anion transporter/exch...	84	4e-16	L
gi 11022647 dbj BAB17026.1	sulfate transporter-like protei...	84	6e-16	
gi 15230510 ref NP_187858.1	sulphate transporter, putative...	83	9e-16	
gi 12711666 ref NP_075062.1	solute carrier family 26, memb...	83	1e-15	L
gi 20336277 ref NP_599025.1	solute carrier family 26, memb...	83	1e-15	L
gi 17389289 gb AAH17697.1 AAH17697	solute carrier family 26...	83	1e-15	L
gi 20140224 sp Q9BXS9 S266 HUMAN	Solute carrier family 26 m...	83	1e-15	
gi 12656494 gb AAK00897.1 AF314819.1	down-regulated in aden...	83	1e-15	
gi 15822827 dbj BAB69041.1	pendrin-like protein 1 [Homo sa...	82	2e-15	L
gi 20336279 ref NP_602298.1	solute carrier family 26, memb...	82	2e-15	L
gi 20162451 gb AAM14591.1 AF493793.1	putative sulphate tran...	82	2e-15	
gi 20867591 ref XP_125957.1	similar to putative anion tran...	82	2e-15	L
gi 10946676 ref NP_067328.1	solute carrier family 26, memb...	81	5e-15	L
gi 24666186 ref NP_649024.1	CG5485-PA [Drosophila melanoga...	80	7e-15	
gi 16197734 emb CAC94921.1	sulfate transporter [Brassica n...	80	8e-15	
gi 17562580 ref NP_505990.1	sulphate transporter [Caenorha...	80	1e-14	L
gi 20162447 gb AAM14589.1	putative sulphate transporter [O...	79	2e-14	
gi 22477993 gb AAH37066.1	Unknown (protein for MGC:46833) ...	77	6e-14	
gi 21294907 gb EAA07052.1	agCP7199 [Anopheles gambiae str....	77	6e-14	
gi 24414264 gb AAAN59767.1	Putative sulfate transporter [Or...	77	9e-14	
gi 20162445 gb AAM14588.1 AF493790.1	putative sulphate tran...	77	9e-14	
gi 24651250 ref NP_651761.1	CG7912-PA [Drosophila melanoga...	76	1e-13	
gi 17509447 ref NP_491138.1	sulfate transporter [Caenorhab...	75	2e-13	L

gi	21296657	gb	EAA08802.1	agCP7781 [Anopheles gambiae str....	75	3e-13	
gi	21295087	gb	EAA07232.1	agCP10636 [Anopheles gambiae str....	75	3e-13	
gi	19922482	ref	NP 611262.1	CG5002-PA [Drosophila melanoga...	74	4e-13	
gi	13487717	gb	AAK27688.1	sulfate transporter 2 [Lycopersi...	74	4e-13	
gi	20336288	ref	NP 599152.1	solute carrier family 26, memb...	74	4e-13	
gi	16418413	ref	NP 443166.1	solute carrier family 26, memb...	74	5e-13	
gi	21294995	gb	EAA07140.1	agCP10674 [Anopheles gambiae str....	74	8e-13	
gi	1711617	sp	P53392 SUT2 STYHA	High affinity sulphate tran...	73	1e-12	
gi	1711615	sp	P53391 SUT1 STYHA	High affinity sulphate tran...	73	1e-12	
gi	13812081	ref	NP 113218.1	sulfate permease [Guillardia t...	73	1e-12	
gi	16197732	emb	CAC94920.1	sulfate transporter [Brassica n...	72	2e-12	
gi	21357695	ref	NP 648539.1	CG6928-PB [Drosophila melanoga...	72	2e-12	
gi	12858334	dbj	BAB31279.1	data source:MGD, source key:MGI...	72	3e-12	
gi	25051587	ref	XP 194484.1	solute carrier family 26, memb...	72	3e-12	
gi	17567633	ref	NP 509424.1	sulfate permease [Caenorhabdit...	71	5e-12	
gi	6502994	gb	AAF14540.1	AF163975 1 Suta [Penicillium chrys...	70	6e-12	
gi	1169148	sp	P23622 CY14 NEUCR	Sulfate permease II	70	1e-11	
gi	18411776	ref	NP 565166.1	high affinity sulphate transpo...	69	1e-11	
gi	15233255	ref	NP 188220.1	putative sulfate transporter; ...	69	1e-11	
gi	15236537	ref	NP 192602.1	putative sulfate transporter; ...	69	1e-11	
gi	11279063	pir	T51839	sulfate transport protein [imported...	69	1e-11	
gi	7489443	pir	T05742	sulfate transport protein, high affi...	69	2e-11	
gi	18395079	ref	NP 564159.1	high affinity sulphate transpo...	69	2e-11	
gi	14270243	emb	CAC39420.1	sulfate transporter [Brassica n...	69	2e-11	
gi	9280683	gb	AAF86552.1	AC069252 11 F2E2.22 [Arabidopsis t...	69	3e-11	
gi	21298441	gb	EAA10586.1	agCP4408 [Anopheles gambiae str....	69	3e-11	
gi	11907976	gb	AAG41419.1	AF309643 1 high affinity sulfate ...	68	3e-11	
gi	15238085	ref	NP 196580.1	sulfate transporter; protein i...	68	3e-11	
gi	22761212	dbj	BAC11496.1	unnamed protein product [Homo s...	68	3e-11	
gi	23273536	gb	AAH35900.1	Unknown (protein for MGC:46523) ...	68	3e-11	
gi	2967454	dbj	BAA25174.1	sulfate transporter [Arabidopsis...	68	3e-11	
gi	18411773	ref	NP 565165.1	sulfate transporter, putative;...	68	3e-11	
gi	24414263	gb	AAN59766.1	Putative sulfate transporter [Or...	68	3e-11	
gi	24047243	gb	AAH38604.1	Unknown (protein for IMAGE:49230...	68	4e-11	
gi	7488356	pir	S74246	sulfate transport protein - Arabidop...	68	4e-11	
gi	22122375	ref	NP 666059.1	hypothetical protein MGC30955 ...	68	4e-11	
gi	13487715	gb	AAK27687.1	sulfate transporter 1 [Lycopersi...	67	5e-11	
gi	20914249	ref	XP 137916.1	similar to CG7912 gene product...	67	5e-11	
gi	14484936	gb	AAK62820.1	high affinity sulfate transporte...	67	5e-11	
gi	15235467	ref	NP 192179.1	sulfate transporter protein; p...	67	6e-11	
gi	16551583	dbj	BAB71126.1	unnamed protein product [Homo s...	67	7e-11	
gi	6502992	gb	AAF14539.1	AF163974 1 sulfate permease SutB [...	67	9e-11	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|20140248|sp|Q9H2B4|S261 HUMAN Sulfate anion transporter 1 (SAT-1)  
gi|10719650|gb|AAG22075.1|AF297659 1 sulfate/anion transporter SAT-1 protein [Ho  
Length = 701

Score = 234 bits (596), Expect = 4e-61

Identities = 126/150 (84%), Positives = 126/150 (84%)

Query: 1 MDSEPEPLXXXXXXXXXXXXXXXXXXLREMLKARLWXXXXXXXXVLCVRALVQDLLPATRWL 60  
MDSEPEPL LREMLKARLW VLCVRALVQDLLPATRWL  
Sbjct: 1 MDSEPEPLQQGRGPVVRQRPAAPRGLREMLKARLWCSCSCSVLCVRALVQDLLPATRWL 60

Query: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120  
RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH  
Sbjct: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

Query: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ  
 Sbjct: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150

☐ >gi|20336272|ref|NP\_071325.2| solute carrier family 26, member 1, isoform a; su  
 transporter SAT-1 protein; sulfate transporter [Homo  
 sapiens]  
 Length = 701

Score = 233 bits (595), Expect = 4e-61  
 Identities = 126/150 (84%), Positives = 126/150 (84%)

Query: 1 MDESPEPLXXXXXXXXXXXXXXXXXXXXLREMLKARLWXXXXXXXXVLCVRLVQDLLPATRWL 60  
 MDESPEPL LREMLKARLW VLCVRLVQDLLPATRWL  
 Sbjct: 1 MDESPEPLQQGRGPVPRRQRPAPRGLREMLKARLWCSCSCSVLCVRLVQDLLPATRWL 60

Query: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120  
 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH  
 Sbjct: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

Query: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ  
 Sbjct: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150

☐ >gi|20336274|ref|NP\_602297.1| solute carrier family 26, member 1, isoform b; su  
 transporter SAT-1 protein; sulfate transporter [Homo  
 sapiens]  
 gi|15930164|gb|AAH15517.1|AAH15517 Similar to solute carrier family 26 (sulfate  
 [Homo sapiens]  
 Length = 224

Score = 232 bits (591), Expect = 1e-60  
 Identities = 126/150 (84%), Positives = 126/150 (84%)

Query: 1 MDESPEPLXXXXXXXXXXXXXXXXXXXXLREMLKARLWXXXXXXXXVLCVRLVQDLLPATRWL 60  
 MDESPEPL LREMLKARLW VLCVRLVQDLLPATRWL  
 Sbjct: 1 MDESPEPLQQGRGPVPRRQRPAPRGLREMLKARLWCSCSCSVLCVRLVQDLLPATRWL 60

Query: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120  
 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH  
 Sbjct: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

Query: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ  
 Sbjct: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150

☐ >gi|11560117|ref|NP\_071623.1| sulfate anion transporter [Rattus norvegicus]  
 gi|1173364|sp|P45380|S261 RAT Sulfate anion transporter 1 (SAT-1) (Canalicular su  
 transporter) (Sulfate/carbonate antiporter)  
 gi|1083806|pir|A49994 sulfate transporter, canalicular - rat  
 gi|431453|gb|AAA17545.1| sulfate anion transporter  
 Length = 703

Score = 197 bits (500), Expect = 4e-50  
 Identities = 109/150 (72%), Positives = 113/150 (75%)

Query: 1 MDESPEPLXXXXXXXXXXXXXXXXXXXXLREMLKARLWXXXXXXXXVLCVRLVQDLLPATRWL 60  
 MD SPEP L E LKARL + C +ALVQ L P RWL  
 Sbjct: 1 MDASPEPPQKGGTLVLVRRQPPVSQGLLETLKARLKKSCSMPCAQALVQGLFPVIRWL 60

Query: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120  
 QYR +EYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH  
 Sbjct: 61 PQYRLKEYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

Query: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 V+VGIFSLCLMVGQVVDRELQLAGFDPSQ  
 Sbjct: 121 VNVGIFSLCLMVGQVVDRELQLAGFDPSQ 150

☐ >gi|19070535|gb|AAL83908.1|AF349043.1 sulfate anion transporter-1 SLC26A1 [Mus]  
 Length = 704

Score = 196 bits (499), Expect = 6e-50  
 Identities = 109/150 (72%), Positives = 113/150 (75%)

Query: 1 MDESPEPLXXXXXXXXXXXXXXXXXXREMLKARLWXXXXXXXXVLCVRALVQDLLPATRWL 60  
 MD SPEP L E LKARL + C +ALVQ L PA WL  
 Sbjct: 1 MDASPEPQQKGGTLVLVRRQPPVSQGLLET LKARLKKSC TCSMPCAQALVQGLFP AIHWL 60

Query: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120  
 QYR +EYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH  
 Sbjct: 61 PQYRLKEYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

Query: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 V+VGIFSLCLMVGQVVDRELQLAGFDPSQ  
 Sbjct: 121 VNVGIFSLCLMVGQVVDRELQLAGFDPSQ 150

☐ >gi|20838541|ref|XP\_132232.1| similar to sulfate anion transporter-1 [Mus muscu  
 gi|20140013|sp|P58735|S261 MOUSE Sulfate anion transporter 1 (SAT-1)  
 gi|18381138|gb|AAH22130.1| Similar to sulfate anion transporter [Mus musculus]  
 gi|19387939|gb|AAH25824.1| Unknown (protein for MGC:37868) [Mus musculus]  
 gi|21618963|gb|AAH32151.1| Unknown (protein for MGC:29387) [Mus musculus]  
 Length = 704

Score = 196 bits (499), Expect = 6e-50  
 Identities = 109/150 (72%), Positives = 113/150 (75%)

Query: 1 MDESPEPLXXXXXXXXXXXXXXXXXXREMLKARLWXXXXXXXXVLCVRALVQDLLPATRWL 60  
 MD SPEP L E LKARL + C +ALVQ L PA WL  
 Sbjct: 1 MDASPEPQQKGGTLVLVRRQPPVSQGLLET LKARLKKSC TCSMPCAQALVQGLFP AIHWL 60

Query: 61 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120  
 QYR +EYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH  
 Sbjct: 61 PQYRLKEYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

Query: 121 VSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 V+VGIFSLCLMVGQVVDRELQLAGFDPSQ  
 Sbjct: 121 VNVGIFSLCLMVGQVVDRELQLAGFDPSQ 150

☐ >gi|6746349|emb|CAB69640.1| DTD sulfate transporter [Bos taurus]  
 Length = 734

Score = 142 bits (357), Expect = 1e-33  
 Identities = 64/94 (68%), Positives = 83/94 (88%)

Query: 54 LPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYF 113  
 LP +WL +Y ++ + GDVMSGL++GI+LVPQ+IAYSLLAG +PIY LYTSFFA+LIYF  
 Sbjct: 94 LPVLQWL PKYDLKKNILGDVMSGLVIGIILVPQSIAYSLLAGQEPIYGLYTSFFASLIYF 153

Query: 114 LMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFD 147  
 ++GTSRH+SVGIF +LCLM+G+VVDREL +AG+D  
 Sbjct: 154 ILGTSRHISVGIFGILCLMIGEVDRELYIAGYD 187

☐ >gi|627422|pir|A54808 diastrophic dysplasia-associated sulfate transport protei  
 Length = 739

Score = 141 bits (356), Expect = 2e-33  
 Identities = 63/99 (63%), Positives = 84/99 (84%)

Query: 49 LVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFA 108  
 ++ LP +WL +Y ++ + GDVMSGL++GI+LVPQ+IAYSLLAG +P+Y LYTSFFA  
 Sbjct: 88 MILGFLPVLQWLPKYDLKKNILGDVMSGLVIGILLVPQSIAYSLLAGQEPVYGLYTSFFA 147

Query: 109 NLIYFLMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFD 147  
 ++IYFL+GTSRH+SVGIF +LCLM+G+ VDRELQ AG+D  
 Sbjct: 148 SIIYFLLGTSRHISVGIFGVLCLMIGETVDRELQKAGYD 186

☐ >gi|4557539|ref|NP\_000103.1| sulfate anion transporter 1; Diastrophic dysplasia transporter [Homo sapiens]  
 gi|1706534|sp|P50443|DTD HUMAN Sulfate transporter (Diastrophic dysplasia protein  
 gi|549988|gb|AAA70081.1| sulfate transporter  
 Length = 739

Score = 141 bits (356), Expect = 2e-33  
 Identities = 63/99 (63%), Positives = 84/99 (84%)

Query: 49 LVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFA 108  
 ++ LP +WL +Y ++ + GDVMSGL++GI+LVPQ+IAYSLLAG +P+Y LYTSFFA  
 Sbjct: 88 MILGFLPVLQWLPKYDLKKNILGDVMSGLVIGILLVPQSIAYSLLAGQEPVYGLYTSFFA 147

Query: 109 NLIYFLMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFD 147  
 ++IYFL+GTSRH+SVGIF +LCLM+G+ VDRELQ AG+D  
 Sbjct: 148 SIIYFLLGTSRHISVGIFGVLCLMIGETVDRELQKAGYD 186

☐ >gi|12054717|emb|CAC20729.1| sulfate transporter [Ovis aries]  
 Length = 734

Score = 140 bits (353), Expect = 5e-33  
 Identities = 63/94 (67%), Positives = 83/94 (88%)

Query: 54 LPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYF 113  
 LP +WL +Y ++ + GD+MSGL++GI+LVPQ+IAYSLLAG +PIY LYTSFFA+LIYF  
 Sbjct: 94 LPVLQWLPKYDLKKNILGDMMMSGLVIGILLVPQSIAYSLLAGQEPYGLYTSFFASLIYF 153

Query: 114 LMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFD 147  
 ++GTSRH+SVGIF +LCLM+G+VVDREL +AG+D  
 Sbjct: 154 ILGTSRHISVGIFGILCLMIGEVVDRELYIAGYD 187

☐ >gi|16923978|ref|NP\_476468.1| solute carrier family 26 (sulfate transporter), m  
 norvegicus]  
 gi|6015035|sp|O70531|DTD RAT Sulfate transporter (Diastrophic dysplasia protein h  
 gi|3123710|dbj|BAA25987.1| sulfate transporter [Rattus norvegicus]  
 Length = 739

Score = 136 bits (343), Expect = 7e-32  
 Identities = 65/118 (55%), Positives = 88/118 (74%)

Query: 27 LREMLKARLWXXXXXXVLCVRLVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQ 86  
 +R+++ +L +R + D P RWL +Y ++ + GD+MSGL++GI+LVPQ  
 Sbjct: 66 IRQLVMRKLQKSCQCNATKIRNRIFDFPVLRLWLPKYDLKKNILGDMMMSGLVIGILLVPQ 125

Query: 87 AIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRHVSVGIFSLCLMVGQVVDRELQLA 144  
 +IAYSLLAG +PIY LYTSFFA++IYFL GTSRH+SVGIF +LCLM+G+VVDREL A  
 Sbjct: 126 SIAYSLLAGQEPYGLYTSFFASIIYFLFGTSRHISVGIFGILCLMIGEVVDRELHKA 183

☐ >gi|12840625|dbj|BAB24899.1| data source:MGD, source key:MGI:892977,  
 evidence:ISS-putative-solute carrier family 26 (sulfate  
 transporter), member 2 [Mus musculus]  
 Length = 225

Score = 136 bits (343), Expect = 7e-32  
 Identities = 63/93 (67%), Positives = 78/93 (83%)

Query: 52 DLLPATRWLRQYRPREYLAGDVMSGLVIGIILVLPQAIAYSLLAGLQPIYSLYTSFFANLI 111  
 D P RWL +Y ++ + GDVMSGL++GI+LVPQ+IAYSLLAG +PIY LYTSFFA++I  
 Sbjct: 91 DFFPVLRLWLPKYDLKKNILGDVMSGLVIGILLVLPQSIAYSLLAGQEPIYVLYTSFFASII 150

Query: 112 YFLMGTSRHVSVGIFSLCLMVGQVVDRELQLA 144  
 YFL GTSRH+SVGIF +LCLM+G+VVDREL A  
 Sbjct: 151 YFLFGTSRHISVGIFGILCLMIGEVDRELHKA 183

☐ >gi|6681233|ref|NP\_031911.1| solute carrier family 26 (sulfate transporter), me  
 diastrophic dysplasia [Mus musculus]  
 gi|2842647|sp|Q62273|DTD MOUSE Sulfate transporter (Diastrophic dysplasia protein  
 gi|575895|dbj|BAA07650.1| sulfate transporter [Mus musculus]  
 Length = 739

Score = 135 bits (341), Expect = 1e-31  
 Identities = 63/93 (67%), Positives = 78/93 (83%)

Query: 52 DLLPATRWLRQYRPREYLAGDVMSGLVIGIILVLPQAIAYSLLAGLQPIYSLYTSFFANLI 111  
 D P RWL +Y ++ + GDVMSGL++GI+LVPQ+IAYSLLAG +PIY LYTSFFA++I  
 Sbjct: 91 DFFPVLRLWLPKYDLKKNILGDVMSGLVIGILLVLPQSIAYSLLAGQEPIYGLYTSFFASII 150

Query: 112 YFLMGTSRHVSVGIFSLCLMVGQVVDRELQLA 144  
 YFL GTSRH+SVGIF +LCLM+G+VVDREL A  
 Sbjct: 151 YFLFGTSRHISVGIFGILCLMIGEVDRELHKA 183

☐ >gi|20306204|gb|AAH28345.1| solute carrier family 26 (sulfate transporter), memb  
 musculus]  
 Length = 739

Score = 135 bits (341), Expect = 1e-31  
 Identities = 63/93 (67%), Positives = 78/93 (83%)

Query: 52 DLLPATRWLRQYRPREYLAGDVMSGLVIGIILVLPQAIAYSLLAGLQPIYSLYTSFFANLI 111  
 D P RWL +Y ++ + GDVMSGL++GI+LVPQ+IAYSLLAG +PIY LYTSFFA++I  
 Sbjct: 91 DFFPVLRLWLPKYDLKKNILGDVMSGLVIGILLVLPQSIAYSLLAGQEPIYGLYTSFFASII 150

Query: 112 YFLMGTSRHVSVGIFSLCLMVGQVVDRELQLA 144  
 YFL GTSRH+SVGIF +LCLM+G+VVDREL A  
 Sbjct: 151 YFLFGTSRHISVGIFGILCLMIGEVDRELHKA 183

☐ >gi|18560370|ref|XP\_087654.1| similar to Sulfate transporter (Diastrophic dyspl  
 [Homo sapiens]  
 Length = 121

Score = 119 bits (297), Expect = 1e-26  
 Identities = 55/74 (74%), Positives = 69/74 (93%)

Query: 74 MSGLVIGIILVLPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRHVSVGIFSLCLMV 133  
 MSGL++GI+LVPQ+IAYSLLAG +P+Y LYTSFFA++IYFL+GTSRH+SVGIF +LCLM+  
 Sbjct: 1 MSGLVIGILLVLPQSIAYSLLAGQEPVYGLYTSFFASIIYFLLGTSRHISVGIFGVLCMI 60

Query: 134 GQVVDRELQLAGFD 147  
 G+ VDRELQ AG+D  
 Sbjct: 61 GETVDRELQKAGYD 74

☐ >gi|23491578|dbj|BAC16761.1| solute carrier family 26 member 6 [Anguilla japonic  
 Length = 754

Score = 93.6 bits (231), Expect = 6e-19  
 Identities = 47/112 (41%), Positives = 72/112 (64%)

Query: 28 REMLKARLWXXXXXXXXVLCVRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVLPQA 87  
 + +L RL V ++ V LP WL +Y R+ GD++SG+ +GI+ +PQ

Sbjct: 31 KPVLVDRLKDSLRCVPRCLKRSVLGCLPVLWSLPRYSIRDCALGDLISGISVGIMHLPQG 90

Query: 88 IAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRHVSVGIFSLLCMLVGVQVDR 139  
+AY+LLA + P++ LYTSF+ L+YF GTSRH+SVG F+++ +MVG V +R

Sbjct: 91 MAYALLASVPPVFGLYTSFYFVPLVYFFFGTSRHHISVGTFVAVSVMVGGVTER 142

☐ >gi|20139418|sp|P58743|PRES HUMAN Prestin  
Length = 744

Score = 93.2 bits (230), Expect = 8e-19  
Identities = 39/94 (41%), Positives = 69/94 (73%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105  
+R ++ LP T+WL Y+ +EY+ GD++SG+ G++ +PQ +A+++LA + PI+ LY+S

Sbjct: 57 IRNIIYMFLPITKWLPAKFKKEYVLGDLVSGISTGVLQLPQGLAFAMLAAPVPIFGLYSS 116

Query: 106 FFANLIYFLMGTSRHVSVGIFSLLCMLVGVQVDR 139  
F+ ++Y +GTSRH+S+G F+++ LM+G V R

Sbjct: 117 FYPVIMYCFLGTSRHHISIGPFAVISLMIGGVAVR 150

☐ >gi|13540646|ref|NP\_110467.1| prestin [Rattus norvegicus]  
gi|20139324|sp|Q9EPH0|PRES RAT Prestin  
gi|12188918|emb|CAC21555.1| prestin [Rattus norvegicus]  
Length = 744

Score = 92.8 bits (229), Expect = 1e-18  
Identities = 39/94 (41%), Positives = 68/94 (72%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105  
VR ++ LP T+WL Y+ +EY+ GD++SG+ G++ +PQ +A+++LA + P++ LY+S

Sbjct: 57 VRNIIYMFLPITKWLPAKFKKEYVLGDLVSGISTGVLQLPQGLAFAMLAAPVPPVFGLYSS 116

Query: 106 FFANLIYFLMGTSRHVSVGIFSLLCMLVGVQVDR 139  
F+ ++Y GTSRH+S+G F+++ LM+G V R

Sbjct: 117 FYPVIMYCFFGTSRHHISIGPFAVISLMIGGVAVR 150

☐ >gi|15011891|ref|NP\_109652.2| prestin (motor protein) [Mus musculus]  
gi|20139650|sp|Q99NH7|PRES MOUSE Prestin  
gi|14787223|gb|AAG59999.2| prestin [Mus musculus]  
Length = 744

Score = 92.4 bits (228), Expect = 2e-18  
Identities = 38/94 (40%), Positives = 68/94 (72%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105  
+R ++ LP T+WL Y+ +EY+ GD++SG+ G++ +PQ +A+++LA + P++ LY+S

Sbjct: 57 IRNIIYMFLPITKWLPAKFKKEYVLGDLVSGISTGVLQLPQGLAFAMLAAPVPPVFGLYSS 116

Query: 106 FFANLIYFLMGTSRHVSVGIFSLLCMLVGVQVDR 139  
F+ ++Y GTSRH+S+G F+++ LM+G V R

Sbjct: 117 FYPVIMYCFFGTSRHHISIGPFAVISLMIGGVAVR 150

☐ >gi|20139749|sp|Q9JKQ2|PRES MERUN Prestin  
gi|8050590|gb|AAF71715.1|AF230376.1 prestin [Meriones unguiculatus]  
Length = 744

Score = 92.4 bits (228), Expect = 2e-18  
Identities = 38/94 (40%), Positives = 68/94 (72%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105  
+R ++ LP T+WL Y+ +EY+ GD++SG+ G++ +PQ +A+++LA + P++ LY+S

Sbjct: 57 IRNIIYMFLPITKWLPAKFKKEYVLGDLVSGISTGVLQLPQGLAFAMLAAPVPPVFGLYSS 116

Query: 106 FFANLIYFLMGTSRHVSVGIFSLLCMLVGVQVDR 139



F+ ++Y GTSRH+S+G F+++ LM+G V R  
 Sbjct: 117 FYPVIMYCFGTSRHSIGPFAVISLMIGGVAVR 150

☐ >gi|17566848|ref|NP\_505493.1| sulphate permease [Caenorhabditis elegans]  
 gi|7511079|pir|T27820| hypothetical protein ZK287.2 - Caenorhabditis elegans  
 gi|3881646|emb|CAA94798.1| Hypothetical protein ZK287.2 [Caenorhabditis elegans]  
 Length = 611

Score = 92.0 bits (227), Expect = 2e-18  
 Identities = 40/88 (45%), Positives = 64/88 (72%)

Query: 47 RALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSF 106  
 R +Q +P WL Y+ +++ GDV++GL +GI+ VPQ +AY+ LAG+ P+Y +Y+SF  
 Sbjct: 25 RKKLQKYIPILEWLPNYQWKDHFHGDVIAGLTVGIMHVPQGMAYASLAGVPPVYGYSSSF 84

Query: 107 FANLIYFLMGTSRHVSVGIFSLCLMVG 134  
 FA+ IY GT+RH+S+G+F++ +MVG  
 Sbjct: 85 FASTIYMFFGTARHSIGVFASMMVG 112

☐ >gi|17570247|ref|NP\_509855.1| dra like protein [Caenorhabditis elegans]  
 gi|7508977|pir|T26165| hypothetical protein W04G3.6 - Caenorhabditis elegans  
 gi|3880488|emb|CAA92028.1| Hypothetical protein W04G3.6 [Caenorhabditis elegans]  
 Length = 380

Score = 91.3 bits (225), Expect = 3e-18  
 Identities = 40/84 (47%), Positives = 60/84 (71%)

Query: 51 QDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANL 110  
 ++ +P T+WL Y E L D++ G+ +GI+ VPQ +AY+ L GL+P+Y LYTS F +L  
 Sbjct: 10 KNYIPITKWLPNYSISENLINDIIGGVTVGILNVPQGMAYASLVGLKPVYGLYTSLFPSL 69

Query: 111 IYFLMGTSRHVSVGIFSLCLMVG 134  
 IY GTSRHV++G+F+++ LM G  
 Sbjct: 70 IYMFFGTSRHVALGVFAVVSLSMSG 93

☐ >gi|17551690|ref|NP\_508944.1| sulfate transporter [Caenorhabditis elegans]  
 gi|14574081|gb|AAA82335.2| Hypothetical protein F14D12.5 [Caenorhabditis elegans]  
 Length = 652

Score = 89.7 bits (221), Expect = 9e-18  
 Identities = 40/105 (38%), Positives = 68/105 (64%), Gaps = 1/105 (0%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105  
 +R ++ +P W+ Y+ + A D ++GL +G+ VPQA++YS+LAGL P+Y LY S  
 Sbjct: 37 IRKIILRRVPVIDWIGSYQINN-ASDFIAGLTMGVYNVPQAMSYILAGLPPVYGLYAS 95

Query: 106 FFANLIYFLMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFDPSQ 150  
 FF +Y + G+++H S+G+FS+ CLMV + V + L+ +P +  
 Sbjct: 96 FFPPFLYSIFGSAKHSSIGVFSITCLMVDKCVKKMLKFRNENPEK 140

☐ >gi|4557535|ref|NP\_000102.1| down-regulated in adenoma protein; down-regulated  
 sapiens]  
 gi|729367|sp|P40879|DRA HUMAN Chloride anion exchanger (DRA protein) (Down-regula  
 gi|2135020|pir|A47456| down-regulated in adenoma (DRA) - human  
 gi|291964|gb|AAA58443.1| Nuclear localization signal at AA 569-573, 576-580, 579  
 transcr. activ. domain 620-640,; homeobox motif 653-676  
 gi|19343676|gb|AAH25671.1| solute carrier family 26, member 3 [Homo sapiens]  
 Length = 764

Score = 89.7 bits (221), Expect = 9e-18  
 Identities = 42/91 (46%), Positives = 59/91 (64%)

Query: 47 RALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSF 106  
 + +V L P WL YR +E+L D++SG+ GI+ V Q +A++LL + P+Y LY SF

Sbjct: 51 KRIVLSLFPIASWLPAYRLKEWLLSDIVSGISTGIVAVLQGLAFALLVDIPPVYGLYASF 110

Query: 107 FANLIYFLMGTSRHVSVGIFSLCLMVGQVV 137

F +IY GTSRH+SVG F +L +MVG V

Sbjct: 111 FPAIIYLFPGTSRHISVGPFPILSMMVGLAV 141

☐ >gi|7499071|pir|T16077 hypothetical protein F14D12.5 - *Caenorhabditis elegans*  
Length = 650

Score = 89.7 bits (221), Expect = 1e-17

Identities = 40/103 (38%), Positives = 67/103 (65%), Gaps = 1/103 (0%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105

+R ++ +P W+ Y+ + A D ++GL +G+ VPQA++YS+LAGL P+Y LY S

Sbjct: 37 IRKIILRRVPVIDWIGSYQINNF-ASDFIAGLTMGVYNVPQAMSYSILAGLPPVYGLYAS 95

Query: 106 FFANLIYFLMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFDP 148

FF +Y + G+++H S+G+FS+ CLMV + V + L+ +P

Sbjct: 96 FPPFLYSIFGSAKHSSIGVFSITCLMVDKCVKKMLKFRNENP 138

☐ >gi|17562578|ref|NP\_505989.1| sulphate transporter [*Caenorhabditis elegans*]  
gi|7505837|pir|T23628 hypothetical protein K12G11.1 - *Caenorhabditis elegans*  
gi|3878554|emb|CAB04606.1| Hypothetical protein K12G11.1 [*Caenorhabditis elegans*]  
Length = 749

Score = 88.6 bits (218), Expect = 2e-17

Identities = 43/104 (41%), Positives = 66/104 (63%)

Query: 46 VRALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTS 105

++ + DL+P +W +Y+ + L+ D++ G+ +G++ VPQ IAY+LLA I LYTS

Sbjct: 87 LKLFIFDLIPILKWFPEYKWKTDLSLDIIGGITVGVMPQGIAYALLAKQPAINGLYTS 146

Query: 106 FFANLIYFLMGTSRHVSVGIFSLCLMVGQVVDRELQLAGFDPS 149

F LIY L GTSRH S+G F+++ LM G V++ +DPS

Sbjct: 147 LFPPLIYMLFGTSRHASLGTFAVSLMTGLSVEKLAAPTIDYDPS 190

☐ >gi|20137595|sp|Q924C9|DRA RAT Chloride anion exchanger (DRA protein) (Down-regu  
gi|15077507|gb|AAK83221.1|AF337809 1 down-regulated in adenoma protein [Rattus n  
Length = 757

Score = 88.2 bits (217), Expect = 3e-17

Identities = 40/93 (43%), Positives = 60/93 (64%)

Query: 47 RALVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSF 106

+ + L P WL Y+ +E+L D++SG+ G++ V Q +A++LL + P Y LY +F

Sbjct: 51 KKIALSLFPIASWLPAYRIKEWLLSDIVSGISTGLVAVLQGLAFALLVNIPPAYGLYAAF 110

Query: 107 FANLIYFLMGTSRHVSVGIFSLCLMVGQVVD 139

F + YF +GTSRH+SVG F +L +MVG VV R

Sbjct: 111 FPVITYFFLGTSRHISVGPFPVLSMMVGVVTR 143

☐ >gi|4505697|ref|NP\_000432.1| pendrin [*Homo sapiens*]  
gi|6174895|sp|O43511|PEND HUMAN Pendrin (Sodium-independent chloride/iodide trans  
gi|2654005|gb|AAC51873.1| pendrin [*Homo sapiens*]  
Length = 780

Score = 86.7 bits (213), Expect = 8e-17

Identities = 42/89 (47%), Positives = 62/89 (69%)

Query: 49 LVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFA 108

+++ L+P WL +YR +E+L DV+SG+ G++ Q +AY+LLA + Y LY+++FF

Sbjct: 64 VLKTLVPILWLPKYRVKEWLLSDVISGVSTGLVATLQGMAYALLAAVPVGYGLYSAFFP 123

Query: 109 NLIYFLMGTSRHVSVGIFSLCLMVGQVV 137

L YF+ GTSRH+SVG F ++ LMVG VV  
 Sbjct: 124 ILTYFIFGTSRHISVGPFVSLMVGSVV 152

☐ >gi|6755022|ref|NP\_035997.1| pendrin; Pendred syndrome homolog (human); Pendred  
 musculus]  
 gi|20139265|sp|Q9R155|PEND MOUSE Pendrin (Sodium-independent chloride/iodide tran  
 gi|5802227|gb|AAD51617.1|AF167411 1 pendrin [Mus musculus]  
 Length = 780

Score = 85.5 bits (210), Expect = 2e-16  
 Identities = 42/89 (47%), Positives = 62/89 (69%)

Query: 49 LVQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFA 108  
 +V+ LLP WL +YR +E+L D++SG+ G++ Q +AY+LLA + + LY++FF  
 Sbjct: 64 VVKTLPLILDWLPKYRVKEWLLSDIISGVSTGLVGTQLQGMAYALLAAVPVQFGLYSAFFP 123

Query: 109 NLIYFLMGTSRHVSVGIFSLCLMVGQVV 137  
 L YF+ GTSRH+SVG F ++ LMVG VV  
 Sbjct: 124 ILTYFVFGTSRHISVGPFVSLMVGSVV 152

☐ >gi|2626753|dbj|BAA23424.1| sulfate transporter [Arabidopsis thaliana]  
 Length = 685

Score = 85.5 bits (210), Expect = 2e-16  
 Identities = 39/88 (44%), Positives = 60/88 (68%)

Query: 50 VQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFAN 109  
 + L P RW+R YR EY D+M+G+ +GI+LVPQA++Y+ LAGL PIY LY+SF  
 Sbjct: 76 IDTLFPCFRWIRTYRWSEYFKLDLMAGITVGIMLVPQAMSYAKLAGLPPIYGLYSSFFVPV 135

Query: 110 LIYFLMGTSRHVSVGIFSLCLMVGQVV 137  
 +Y + G+SR +++G +L+ L+V +  
 Sbjct: 136 FVYAIFGSSRQLAIGPVALVSLVSNAL 163

☐ >gi|15240652|ref|NP\_196859.1| sulfate transporter; protein id: At5g13550.1, supp  
 gi\_2626752 [Arabidopsis thaliana]  
 gi|9955547|emb|CAC05432.1| sulfate transporter [Arabidopsis thaliana]  
 Length = 685

Score = 85.5 bits (210), Expect = 2e-16  
 Identities = 39/88 (44%), Positives = 60/88 (68%)

Query: 50 VQDLLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFAN 109  
 + L P RW+R YR EY D+M+G+ +GI+LVPQA++Y+ LAGL PIY LY+SF  
 Sbjct: 76 IDTLFPCFRWIRTYRWSEYFKLDLMAGITVGIMLVPQAMSYAKLAGLPPIYGLYSSFFVPV 135

Query: 110 LIYFLMGTSRHVSVGIFSLCLMVGQVV 137  
 +Y + G+SR +++G +L+ L+V +  
 Sbjct: 136 FVYAIFGSSRQLAIGPVALVSLVSNAL 163

☐ >gi|9506965|ref|NP\_062087.1| pendrin; Pendred syndrome homolog (human) [Rattus  
 gi|20138820|sp|Q9R154|PEND RAT Pendrin (Sodium-independent chloride/iodide transp  
 gi|5802229|gb|AAD51618.1|AF167412 1 pendrin [Rattus norvegicus]  
 Length = 780

Score = 85.1 bits (209), Expect = 3e-16  
 Identities = 42/85 (49%), Positives = 59/85 (69%)

Query: 53 LLPATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIY 112  
 LLP WL +YR +E+L D++SG+ G++ Q +AY+LLA + Y LY++FF L Y  
 Sbjct: 68 LLPILDWLPKYRVKEWLLSDIISGVSTGLVGTQLQGMAYALLAAVPVQYGLYSAFFPILTY 127

Query: 113 FLMGTSRHVSVGIFSLCLMVGQVV 137  
 F+ GTSRH+SVG F ++ LMVG VV

Sbjct: 128 FVFGTSRHHISVGPFVSLMVGSVV 152

☐ >gi|19705561|ref|NP\_599252.1| solute carrier family 26, member 6 [Mus musculus]  
gi|15080864|gb|AAK51131.1| chloride-formate exchanger [Mus musculus]  
Length = 735

Score = 85.1 bits (209), Expect = 3e-16  
Identities = 49/98 (50%), Positives = 68/98 (69%), Gaps = 4/98 (4%)

Query: 45 CVRALVQDLL----PATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIY 100  
C RA LL P WL +Y RE+L GD++SGL + I+ +PQ +AY+LLAGL P++  
Sbjct: 41 CSRARAHSLLLQHVPVLGWLPRYPXREWLLGDLLSGLSVAIMQLPQGLAYALLAGLPPMF 100

Query: 101 SLYTSFFANLIYFLMGTSRHHVSVGIFSLCLMVGQVVD 138  
LY+SF+ IYFL GTSRH+SVG F+++ +MVG V +

Sbjct: 101 GLYSSFPVFIYFLFGTSRHHISVGTFVMSVMVGSVTE 138

☐ >gi|22775307|gb|AAL13129.1| anion exchanger SLC26A6a [Mus musculus]  
Length = 758

Score = 84.3 bits (207), Expect = 4e-16  
Identities = 49/98 (50%), Positives = 68/98 (69%), Gaps = 4/98 (4%)

Query: 45 CVRALVQDLL----PATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIY 100  
C RA LL P WL +Y RE+L GD++SGL + I+ +PQ +AY+LLAGL P++  
Sbjct: 64 CSRARAHSLLLQHVPVLGWLPRYPVREWLLGDLLSGLSVAIMQLPQGLAYALLAGLPPMF 123

Query: 101 SLYTSFFANLIYFLMGTSRHHVSVGIFSLCLMVGQVVD 138  
LY+SF+ IYFL GTSRH+SVG F+++ +MVG V +

Sbjct: 124 GLYSSFPVFIYFLFGTSRHHISVGTFVMSVMVGSVTE 161

☐ >gi|20810386|gb|AAH28856.1| solute carrier family 26, member 6 [Mus musculus]  
Length = 735

Score = 84.3 bits (207), Expect = 4e-16  
Identities = 49/98 (50%), Positives = 68/98 (69%), Gaps = 4/98 (4%)

Query: 45 CVRALVQDLL----PATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIY 100  
C RA LL P WL +Y RE+L GD++SGL + I+ +PQ +AY+LLAGL P++  
Sbjct: 41 CSRARAHSLLLQHVPVLGWLPRYPVREWLLGDLLSGLSVAIMQLPQGLAYALLAGLPPMF 100

Query: 101 SLYTSFFANLIYFLMGTSRHHVSVGIFSLCLMVGQVVD 138  
LY+SF+ IYFL GTSRH+SVG F+++ +MVG V +

Sbjct: 101 GLYSSFPVFIYFLFGTSRHHISVGTFVMSVMVGSVTE 138

☐ >gi|22773848|gb|AAN07089.1|AF248494.1 anion transporter/exchanger-5 SLC26A6B [M]  
Length = 735

Score = 84.3 bits (207), Expect = 4e-16  
Identities = 49/98 (50%), Positives = 68/98 (69%), Gaps = 4/98 (4%)

Query: 45 CVRALVQDLL----PATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIY 100  
C RA LL P WL +Y RE+L GD++SGL + I+ +PQ +AY+LLAGL P++  
Sbjct: 41 CSRARAHSLLLQHVPVLGWLPRYPVREWLLGDLLSGLSVAIMQLPQGLAYALLAGLPPMF 100

Query: 101 SLYTSFFANLIYFLMGTSRHHVSVGIFSLCLMVGQVVD 138  
LY+SF+ IYFL GTSRH+SVG F+++ +MVG V +

Sbjct: 101 GLYSSFPVFIYFLFGTSRHHISVGTFVMSVMVGSVTE 138

☐ >gi|11022647|dbj|BAB17026.1| sulfate transporter-like protein [Arabidopsis thali]  
Length = 389

Score = 84.0 bits (206), Expect = 6e-16  
Identities = 39/88 (44%), Positives = 60/88 (68%)